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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=7; day=7; hr=13; min=15; sec=48; ms=415;]

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Application No: 10593846 Version No: 1.0

Input Set:

Output Set:

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Finished: 2008-06-30 20:05:24.292
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Total Warnings: 2
Total Errors: 0
No. of SeqIDs Defined: 12
Actual SeqID Count: 12

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
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SEQUENCE LISTING

<110> DIVERSA CORPORATION
 BARTON, Nelson R.
 O'DONOGHUE, Eileen
 SHORT, Ryan
 FREY, Gerhard
 WEINER, David
 ROBERTSON, Dan E.
 BRIGGS, Steven
 ZORNER, Paul

<120> CHIMERIC CANNULAE PROTEINS, NUCLEIC ACIDS ENCODING
 THEM AND METHODS FOR MAKING AND USING THEM

<130> 564462006801

<140> 10593846

<141> 2008-06-30

<150> PCT/US2005/009927

<151> 2005-03-24

<150> 60/556,393

<151> 2004-03-24

<150> 60/605,192

<151> 2004-08-27

<160> 12

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 624

<212> DNA

<213> Pyrodictium abyssi

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ggcgcacagg gcagtgacga cataggttac gcaatagtgt ggataaagga ccaggtcaat	240
gatgtaaagc tgaaggtgac cctgcgtaac gctgagcagc taaagcccta cttcaagtac	300
ctacagatac agataacaag cggtatagag acgaacagca cagctctagg caacttcagc	360
gagaccaagg ctgtgataag cctcgacaac cccagcgccg tgatagtact agacaaggag	420
gatatagcag tgctctatcc ggacaagacc ggttacacaa acacttcgat atgggtaccc	480
ggtgaacctg acaagataat tgtctacaac gagacaaagc cagtagctat actgaacttc	540
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<213> Pyrodictium abyssi

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Ser Phe Tyr Ala Thr Gly Thr Ala Gln Ala Val Ser Glu Pro Ile Asp
      35              40              45
Val Glu Ser His Leu Gly Ser Ile Thr Pro Ala Ala Gly Ala Gln Gly
      50              55              60
Ser Asp Asp Ile Gly Tyr Ala Ile Val Trp Ile Lys Asp Gln Val Asn
      65              70              75              80
Asp Val Lys Leu Lys Val Thr Leu Arg Asn Ala Glu Gln Leu Lys Pro
      85              90              95
Tyr Phe Lys Tyr Leu Gln Ile Gln Ile Thr Ser Gly Tyr Glu Thr Asn
      100             105             110
Ser Thr Ala Leu Gly Asn Phe Ser Glu Thr Lys Ala Val Ile Ser Leu
      115             120             125
Asp Asn Pro Ser Ala Val Ile Val Leu Asp Lys Glu Asp Ile Ala Val
      130             135             140
Leu Tyr Pro Asp Lys Thr Gly Tyr Thr Asn Thr Ser Ile Trp Val Pro
      145             150             155             160
Gly Glu Pro Asp Lys Ile Ile Val Tyr Asn Glu Thr Lys Pro Val Ala
      165             170             175
Ile Leu Asn Phe Lys Ala Phe Tyr Glu Ala Lys Glu Gly Met Leu Phe
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<212> DNA

<213> Pyrodictium abyssi

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gccgcaacaa gcgagccaat agacgtagag agccacctca gcagcatagc ccctgctgct      180
ggcgcacagg gcagccagga cataggctac ttcaacgtga cgcgcaagga tcaagtgaac      240
gtgacaaaga taaaggtgac cctggctaac gctgagcagc taaagcccta cttcaagtac      300
ctacagatag tgctaaagag cgaggtagct gacgagatca aggccgtaat aagcatagac      360
aagcctagcg ccgtcataat actagacagc caggacttcg acagcaacaa cagagcaaag      420
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<213> Pyrodictium abyssi

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      20              25              30
Ser Phe Tyr Ala Thr Gly Thr Ala Ala Ala Thr Ser Glu Pro Ile Asp
      35              40              45
Val Glu Ser His Leu Ser Ser Ile Ala Pro Ala Ala Gly Ala Gln Gly
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Val Thr Lys Ile Lys Val Thr Leu Ala Asn Ala Glu Gln Leu Lys Pro		80
	85	90
Tyr Phe Lys Tyr Leu Gln Ile Val Leu Lys Ser Glu Val Ala Asp Glu		95
	100	105
Ile Lys Ala Val Ile Ser Ile Asp Lys Pro Ser Ala Val Ile Ile Leu		110
	115	120
Asp Ser Gln Asp Phe Asp Ser Asn Asn Arg Ala Lys Ile Ser Ala Thr		125
	130	135
Ala Tyr Tyr Glu Ala Lys Glu Gly Met Leu Phe Asp Ser Leu Pro Leu		140
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<212> DNA

<213> Pyrodictium abyssi

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caagcagtaa gcgagccaat agacgtagag agccacctag acaacacccat agccctgct	180
gccggtgcac agggctacaa ggacatgggc tacattaaga taactaacca gtcaaaagtt	240
aatgtaataa agctgaaggt gactctcgct aacgccgagc agctaaagcc ctacttcgac	300
tacctacagc tagtactcac aagcaacgcc actggcaccg acatgggtaa ggctgtgcta	360
agcctcgaga agcctagcgc agtcataata ctagacaacg atgactacga tagcactaac	420
aagatacagc taaaggtaga agcctactat gaggctaagg agggcatgct attcgacagc	480
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<210> 6

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<212> PRT

<213> Pyrodictium abyssi

<400> 6

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20	30
Ser Phe Tyr Ala Thr Gly Thr Ala Gln Ala Val Ser Glu Pro Ile Asp	
35	45
Val Glu Ser His Leu Asp Asn Thr Ile Ala Pro Ala Ala Gly Ala Gln	
50	60
Gly Tyr Lys Asp Met Gly Tyr Ile Lys Ile Thr Asn Gln Ser Lys Val	
65	80
Asn Val Ile Lys Leu Lys Val Thr Leu Ala Asn Ala Glu Gln Leu Lys	
85	95
Pro Tyr Phe Asp Tyr Leu Gln Leu Val Leu Thr Ser Asn Ala Thr Gly	
100	110
Thr Asp Met Val Lys Ala Val Leu Ser Leu Glu Lys Pro Ser Ala Val	
115	125
Ile Ile Leu Asp Asn Asp Asp Tyr Asp Ser Thr Asn Lys Ile Gln Leu	
130	140
Lys Val Glu Ala Tyr Tyr Glu Ala Lys Glu Gly Met Leu Phe Asp Ser	

145 150 155 160
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 165 170 175
 Leu Trp

<210> 7
 <211> 395
 <212> DNA
 <213> Pyrodictium abyssi

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 atatatgcmc acaatgacgt gaacataaca aagctaaagg tcacgcttgc taacgctgca 180
 cagctaagac catacttcaa gtacctgata ataaagctag taagcctgga cagcaacggc 240
 aacgagtccg aggaaaagg catgataact ctatggaagc cttacgccgt gataatacta 300
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<210> 8
 <211> 131
 <212> PRT
 <213> Pyrodictium abyssi

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 Lys Gln Thr Leu Gly Asp Ile Thr Ile Tyr Ala His Asn Asp Val Asn
 35 40 45
 Ile Thr Lys Leu Lys Val Thr Leu Ala Asn Ala Ala Gln Leu Arg Pro
 50 55 60
 Tyr Phe Lys Tyr Leu Ile Ile Lys Leu Val Ser Leu Asp Ser Asn Gly
 65 70 75 80
 Asn Glu Ser Glu Glu Lys Gly Met Ile Thr Leu Trp Lys Pro Tyr Ala
 85 90 95
 Val Ile Ile Leu Asp His Glu Asp Phe Asn Asn Asp Ile Asp Asn Asp
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 Glu Gly Met
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<210> 9
 <211> 372
 <212> DNA
 <213> Pyrodictium abyssi

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 acaatagaga acaagactga cgtgaacggt gtgaagctga agataaccct cgccaacgct 180
 gagcagctaa agccctactt cgactaccta cagatagtgc taaagagcgt tgacagcaac 240
 gagatcaagg ctgtgctaag cctcgagaag ccagcgcag tcataatact ggacaacgag 300
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 gagggtatgc ta 372

<210> 10
 <211> 124
 <212> PRT
 <213> Pyrodictium abyssi

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 20 25 30
 Gly Ser Val Gly Ile Gly Ser Ile Thr Ile Glu Asn Lys Thr Asp Val
 35 40 45
 Asn Val Val Lys Leu Lys Ile Thr Leu Ala Asn Ala Glu Gln Leu Lys
 50 55 60
 Pro Tyr Phe Asp Tyr Leu Gln Ile Val Leu Lys Ser Val Asp Ser Asn
 65 70 75 80
 Glu Ile Lys Ala Val Leu Ser Leu Glu Lys Pro Ser Ala Val Ile Ile
 85 90 95
 Leu Asp Asn Glu Asp Phe Gln Gly Gly Asp Asn Gln Cys Gln Ile Asp
 100 105 110
 Ala Thr Ala Tyr Tyr Glu Ala Lys Glu Gly Met Leu
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<210> 11
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> consensus sequence

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 acgtagaaaag ccacctcaca catagcccct gctgccggcg cacagggcag caggacatag 180
 gctacataaa ataacaagat agtgaacgta taaagctgaa ggtgaccctg ctaacgctga 240
 gcagctaaag ccctacttca agtacctaca gatagtgtga aaagcgacag caggcacacg 300
 agaaggcgtg ataagcctcg agaagcctag cgccgtcata atactagaca acgaggactt 360
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 <211> 140
 <212> PRT
 <213> Artificial Sequence

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 <223> consensus sequence

<400> 12
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 20 25 30
 Thr Gly Thr Ala Gln Ala Val Ser Glu Pro Ile Asp Val Glu Ser His
 35 40 45

Leu	Ser	Ile	Ala	Pro	Ala	Ala	Gly	Ala	Gln	Gly	Ser	Asp	Ile	Gly	Tyr
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Ile	Ile	Lys	Val	Asn	Val	Val	Lys	Leu	Lys	Val	Thr	Leu	Ala	Asn	Ala
65					70					75					80
Glu	Gln	Leu	Lys	Pro	Tyr	Phe	Lys	Tyr	Leu	Gln	Ile	Val	Leu	Ser	Ser
				85					90					95	
Glu	Ile	Lys	Ala	Val	Ile	Ser	Leu	Asp	Lys	Pro	Ser	Ala	Val	Ile	Ile
			100					105					110		
Leu	Asp	Glu	Asp	Phe	Ala	Ile	Ala	Tyr	Tyr	Glu	Ala	Lys	Glu	Gly	Met
		115					120					125			
Leu	Phe	Asp	Ser	Leu	Pro	Val	Ile	Asn	Gln	Val	Leu				
130						135					140				